

CLAIM AMENDMENTS**Claims 1-27 (canceled)**

Claim 28 (currently amended) A method for detecting a target nucleotide sequence, and providing a partial helical enclosure of the target sequence, comprising the steps of:

- a) rendering the target nucleotide sequence substantially single-stranded;
- (b) hybridizing the single-stranded target nucleotide sequence with a nucleic acid probe unit, comprising: (i) a sequence complementary to the single stranded target nucleotide sequence, and (ii) a probe linker at each of the two terminal ends of the probe unit, said probe linker comprises a single stranded nucleotide sequence that hybridizes to a reporter linker of a reporter but does not hybridize to the single stranded target nucleotide sequence two oligonucleotides that are overlapped end to end to form a linear probe unit prior to target hybridization, wherein the first oligonucleotide comprises three segments sequentially: a first universal probe linker on one end that hybridizes to a universal reporter linker of a reporter but does not bind the single-stranded target nucleotide sequence, a central sequence complementary to the single-stranded target nucleotide sequence, and an overlap linker on the other end; wherein the second oligonucleotide comprises two segments sequentially: a matching overlap linker that is hybridized to the overlap linker of the first

oligonucleotide, and a second universal probe linker which hybridizes to a universal reporter linker of a reporter but does not bind the single-stranded target nucleotide sequence;

- (c) washing to remove any unbound probe;
- (d) hybridizing reporters to the two probe linkers; and
- (e) detecting the presence of the reporter reporters to indicate the presence of the target nucleotide sequence.

Claim 29 (canceled)

Claim 30 (currently amended) The method of claim 28, wherein the reporter comprises a labeled, double stranded polynucleotide sequence linked on one or both ends to a universal reporter linker that comprises a short single-stranded polynucleotide.

Claim 31 (currently amended) The method of claim 30, wherein the double-stranded polynucleotide sequence is at least 100 bases long and the short single-stranded polynucleotide linker is from about 20 bases to about 30 bases long.

Claim 32 (currently amended) The method of claim 30, wherein two or more reporters form a reporter array by linking end-to-end via [[the]] complementary universal reporter linkers.

Claim 33 (currently amended) The method of claim 32, wherein the length of the reporter array is determined by a ratio of terminator oligonucleotide to reporters, said terminator oligonucleotide terminates the reporter array by hybridizing to [[a]] said reporter linker at the end of the reporter array.

Claim 34. (currently amended) The method of claim 32, wherein the reporter array comprises successive layers of type I and type II reporters, each of the type I and type II reporter comprises a first and a second universal reporter linker, wherein the first and the second universal reporter linker of a type I reporter is hybridized respectively to the second universal reporter linker of a type II reporter and to the first universal reporter linker of another type II reporter, except the first universal reporter linker of the type I reporter in the first layer of reporter is hybridized to a universal probe linker of a probe.

Claim 35 (currently amended) The method of claim 28, wherein a multi-linking unit is interposed between the reporter and the probe linker, said multi-linking unit comprises (i) a sequence that hybridizes to the probe linker and (ii) two or more sequences that hybridize to [[the]] said reporter linker of the reporter.

Claims 36-58 (canceled)

Claim 59 (previously presented) The method of claim 29, wherein the overlap linker and or the probe linker comprises one or more TA sequence to facilitate interstrand crosslinking between complementary linkers during probe fabrication or use.

Claim 60 (currently amended) The method of claim 30, wherein [[the]] said universal reporter linker further comprises a carbon spacer segment.

Claim 61. (currently amended) The method of claim 30, wherein the universal reporter linker ~~comprises sequence selected from the group consisting~~ consists of SEQ ID NO. ~~6, 10, 12, 71, 73, 76, 78, 81 and 83.~~